

## RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/655,543A  
Source: 1 Fw/b.  
Date Processed by STIC: 12/27/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 12/27/2006

PATENT APPLICATION: US/10/655,543A

TIME: 13:54:26

Input Set : N:\efs\12\_27\_06\10655543A\_efs\1312-03-2006-12-21-

HLL-ST25.txt

Output Set: N:\CRF4\12272006\J655543A.raw

3 <110> APPLICANT: Shattuck, Donna M.  
 4 Stone, Steven  
 5 Russell, Deanna L  
 6 Abkevich, Victor  
 7 Hunt, Steven  
 9 <120> TITLE OF INVENTION: OBESITY GENE AND USE THEREOF  
 11 <130> FILE REFERENCE: 1312.03  
 13 <140> CURRENT APPLICATION NUMBER: US 10/655,543A  
 14 <141> CURRENT FILING DATE: 2003-09-03  
 16 <160> NUMBER OF SEQ ID NOS: 108  
 18 <170> SOFTWARE: PatentIn version 3.3  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 3507  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
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 30 ccctgggttg tggtgaggt gcgaagactc agcaggcagt ccaccagaaa ggaacctgta 180  
 32 accaagcaag tccggctttg cgtttcaccc tctggactga gatgtgaacc tgagccaggg 240  
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 48 cccacagggg gccaggagcc tgtgcgagg cccatgcgca agtccttctc ccagcccggc 720  
 50 ctgctgctcg tggcctttag gaaggagctg caggatgggg gcctccgaag cagcggcttc 780  
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*see p. 6*

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86 cccatcgaat gccaggaacc tccacaacct gcccgggggt ccccggggggt ttcgcaaagg 1860
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153 1 5 10 15
156 Val Ser Val Asp Phe Gly Leu Gln Leu Val Gly Ser Leu Pro Val His
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160 Ser Leu Thr Thr Met Pro Met Leu Pro Trp Val Val Ala Glu Val Arg
161 35 40 45
164 Arg Leu Ser Arg Gln Ser Thr Arg Lys Glu Pro Val Thr Lys Gln Val
165 50 55 60
168 Arg Leu Cys Val Ser Pro Ser Gly Leu Arg Cys Glu Pro Glu Pro Gly
169 65 70 75 80
172 Arg Ser Gln Gln Trp Asp Pro Leu Ile Tyr Ser Ser Ile Phe Glu Cys
173 85 90 95

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180 Tyr Phe Ala Cys Leu Ile Lys Glu Asp Ala Val His Arg Gln Ser Ile
181      115      120      125
184 Cys Tyr Val Phe Lys Ala Asp Asp Gln Thr Lys Val Pro Glu Ile Ile
185      130      135      140
188 Ser Ser Ile Arg Gln Ala Gly Lys Ile Ala Arg Gln Glu Glu Leu His
189 145      150      155      160
192 Cys Pro Ser Glu Phe Asp Asp Thr Phe Ser Lys Lys Phe Glu Val Leu
193      165      170      175
196 Phe Cys Gly Arg Val Thr Val Ala His Lys Lys Ala Pro Pro Ala Leu
197      180      185      190
200 Ile Asp Glu Cys Ile Glu Lys Phe Asn His Val Ser Gly Ser Arg Gly
201      195      200      205
204 Ser Glu Ser Pro Arg Pro Asn Pro Pro His Ala Ala Pro Thr Gly Ser
205      210      215      220
208 Gln Glu Pro Val Arg Arg Pro Met Arg Lys Ser Phe Ser Gln Pro Gly
209 225      230      235      240
212 Leu Arg Ser Leu Ala Phe Arg Lys Glu Leu Gln Asp Gly Gly Leu Arg
213      245      250      255
216 Ser Ser Gly Phe Phe Ser Ser Phe Glu Glu Ser Asp Ile Glu Asn His
217      260      265      270
220 Leu Ile Ser Gly His Asn Ile Val Gln Pro Thr Asp Ile Glu Glu Asn
221      275      280      285
224 Arg Thr Met Leu Phe Thr Ile Gly Gln Ser Glu Val Tyr Leu Ile Ser
225      290      295      300
228 Pro Asp Thr Lys Lys Ile Ala Leu Glu Lys Asn Phe Lys Glu Ile Ser
229 305      310      315      320
232 Phe Cys Ser Gln Gly Ile Arg His Val Asp His Phe Gly Phe Ile Cys
233      325      330      335
236 Arg Glu Ser Ser Gly Gly Gly Gly Phe His Phe Val Cys Tyr Val Phe
237      340      345      350
240 Gln Cys Thr Asn Glu Ala Leu Val Asp Glu Ile Met Met Thr Leu Lys
241      355      360      365
244 Gln Ala Phe Thr Val Ala Ala Val Gln Gln Thr Ala Lys Ala Pro Ala
245      370      375      380
248 Gln Leu Cys Glu Gly Cys Pro Leu Gln Ser Leu His Lys Leu Cys Glu
249 385      390      395      400
252 Arg Ile Glu Gly Met Asn Ser Ser Lys Thr Lys Leu Glu Leu Gln Lys
253      405      410      415
256 His Leu Thr Thr Leu Thr Asn Gln Glu Gln Ala Thr Ile Phe Glu Glu
257      420      425      430
260 Val Gln Lys Leu Arg Pro Arg Asn Glu Gln Arg Glu Asn Glu Leu Ile
261      435      440      445
264 Ile Ser Phe Leu Arg Cys Leu Tyr Glu Glu Lys Gln Lys Glu His Ile
265      450      455      460
268 His Ile Gly Glu Met Lys Gln Thr Ser Gln Met Ala Ala Glu Asn Ile
269 465      470      475      480
272 Gly Ser Glu Leu Pro Pro Ser Ala Thr Arg Phe Arg Leu Asp Met Leu

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280	Ser	Arg	Gly	Asn	Lys	Ala	Arg	Gly	Leu	Gln	Glu	His	Ser	Ile	Ser	Val
281			515					520				525				
284	Asp	Leu	Asp	Ser	Ser	Leu	Ser	Ser	Thr	Leu	Ser	Asn	Thr	Ser	Lys	Glu
285		530					535				540					
288	Pro	Ser	Val	Cys	Glu	Lys	Glu	Ala	Leu	Pro	Ile	Ser	Glu	Ser	Ser	Phe
289	545					550				555						560
292	Lys	Leu	Leu	Gly	Ser	Ser	Glu	Asp	Leu	Ser	Ser	Asp	Ser	Glu	Ser	His
293				565				570				575				
296	Leu	Pro	Glu	Glu	Pro	Ala	Pro	Leu	Ser	Pro	Gln	Gln	Ala	Phe	Arg	Arg
297			580					585				590				
300	Arg	Ala	Asn	Thr	Leu	Ser	His	Phe	Pro	Ile	Glu	Cys	Gln	Glu	Pro	Pro
301			595					600				605				
304	Gln	Pro	Ala	Arg	Gly	Ser	Pro	Gly	Val	Ser	Gln	Arg	Lys	Leu	Met	Arg
305		610					615				620					
308	Tyr	His	Ser	Val	Ser	Thr	Glu	Thr	Pro	His	Glu	Arg	Lys	Asp	Phe	Glu
309	625					630				635						640
312	Ser	Lys	Ala	Asn	His	Leu	Gly	Asp	Ser	Gly	Gly	Thr	Pro	Val	Lys	Thr
313				645				650				655				
316	Arg	Arg	His	Ser	Trp	Arg	Gln	Gln	Ile	Phe	Leu	Arg	Val	Ala	Thr	Pro
317			660					665				670				
320	Gln	Lys	Ala	Cys	Asp	Ser	Ser	Ser	Arg	Tyr	Glu	Asp	Tyr	Ser	Glu	Leu
321			675					680				685				
324	Gly	Glu	Leu	Pro	Pro	Arg	Ser	Pro	Leu	Glu	Pro	Val	Cys	Glu	Asp	Gly
325		690					695				700					
328	Pro	Phe	Gly	Pro	Pro	Pro	Glu	Glu	Lys	Lys	Arg	Thr	Ser	Arg	Glu	Leu
329	705					710				715						720
332	Arg	Glu	Leu	Trp	Gln	Lys	Ala	Ile	Leu	Gln	Gln	Ile	Leu	Leu	Leu	Arg
333			725					730				735				
336	Met	Glu	Lys	Glu	Asn	Gln	Lys	Leu	Gln	Ala	Ser	Glu	Asn	Asp	Leu	Leu
337			740					745				750				
340	Asn	Lys	Arg	Leu	Lys	Leu	Asp	Tyr	Glu	Glu	Ile	Thr	Pro	Cys	Leu	Lys
341			755					760				765				
344	Glu	Val	Thr	Thr	Val	Trp	Glu	Lys	Met	Leu	Ser	Thr	Pro	Gly	Arg	Ser
345		770					775				780					
348	Lys	Ile	Lys	Phe	Asp	Met	Glu	Lys	Met	His	Ser	Ala	Val	Gly	Gln	Gly
349	785					790				795						800
352	Val	Pro	Arg	His	His	Arg	Gly	Glu	Ile	Trp	Lys	Phe	Leu	Ala	Glu	Gln
353				805				810								815
356	Phe	His	Leu	Lys	His	Gln	Phe	Pro	Ser	Lys	Gln	Gln	Pro	Lys	Asp	Val
357			820					825				830				
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361			835					840				845				
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380 Leu Lys Phe Leu Met Phe Asp Met Gly Leu Arg Lys Gln Tyr Arg Pro
381           915           920           925
384 Asp Met Ile Ile Leu Gln Ile Gln Met Tyr Gln Leu Ser Arg Leu Leu
385           930           935           940
388 His Asp Tyr His Arg Asp Leu Tyr Asn His Leu Glu Glu His Glu Ile
389 945           950           955           960
392 Gly Pro Ser Leu Tyr Ala Ala Pro Trp Phe Leu Thr Met Phe Ala Ser
393           965           970           975
396 Gln Phe Pro Leu Gly Phe Val Ala Arg Val Phe Asp Met Ile Phe Leu
397           980           985           990
400 Gln Gly Thr Glu Val Ile Phe Lys Val Ala Leu Ser Leu Leu Gly Ser
401           995           1000           1005
404 His Lys Pro Leu Ile Leu Gln His Glu Asn Leu Glu Thr Ile Val
405           1010           1015           1020
408 Asp Phe Ile Lys Ser Thr Leu Pro Asn Leu Gly Leu Val Gln Met
409           1025           1030           1035
412 Glu Lys Thr Ile Asn Gln Val Phe Glu Met Asp Ile Ala Lys Gln
413           1040           1045           1050
416 Leu Gln Ala Tyr Glu Val Glu Tyr His Val Leu Gln Glu Glu Leu
417           1055           1060           1065
420 Ile Asp Ser Ser Pro Leu Ser Asp Asn Gln Arg Met Asp Lys Leu
421           1070           1075           1080
424 Glu Lys Thr Asn Ser Ser Leu Arg Lys Gln Asn Leu Asp Leu Leu
425           1085           1090           1095
428 Glu Gln Leu Gln Val Ala Asn Gly Arg Ile Gln Ser Leu Glu Ala
429           1100           1105           1110
432 Thr Ile Glu Lys Leu Leu Ser Ser Glu Ser Lys Leu Lys Gln Ala
433           1115           1120           1125
436 Met Leu Thr Leu Glu Leu Glu Arg Ser Ala Leu Leu Gln Thr Val
437           1130           1135           1140
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458 cctgggttg tggctgaggt gcgaagactc agcaggcagt ccaccagaaa ggaacctgta      180
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RAW SEQUENCE LISTING ERROR SUMMARY  
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*FyI*  
Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; Xaa Pos. 59,520,525

VERIFICATION SUMMARY

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